IN THE SPECIFICATION:

Please replace the paragraph beginning at Page 31, Line 13 with the following rewritten paragraph:

Figures 1A-~~1F~~1G show the nucleotide ~~[SEQ ID NO:1]~~(SEQ ID NO: 1) and predicted amino acid ~~[SEQ ID NO:2]~~(SEQ ID NO: 2) sequence of murine NR4. The untranslated region is shown in lower case and the translated region in upper case. The conventional one-letter code for amino acids is employed, potential asparagine linked glycosylation sites are underlined and the conserved cysteine residues and WSXWS (SEQ ID NO: 12) motif of haempoietin receptor family members are shown in bold. The predicted signal sequence is underlined in bold while the transmembrane domain is underlined with dashes. The sequence shown is a composite derived from the analysis of 8 cDNA clones derived from 3 libraries. The 5'-end of the sequence (nucleotides –60 to 351) is derived from a single cDNA clone but is also present in genomic DNA clones that have been isolated. Boxed region – typical haempoietin receptor domain, amino acids 118-340.

Please replace the paragraph beginning at Page 32, Line 3 with the following rewritten paragraph:

Figures 7A-~~7J~~7K show the nucleotide and corresponding amino acid sequence of murine (SEQ ID NOs: 1 and 2, respectively) and human (SEQ ID NOs: 3 and 4, respectively) NR4 (IL-13Rα) genes. The nucleotide and predicted amino acid sequence of human (H) and murine (M) IL-13Rα (NR4) were aligned by eye, with gaps (-) inserted to optimize the alignment. The numbering is for the murine clone, nucleotides that form part of the coding region are shown in upper case, whilst those of the untranslated regions are shown in lower case. Amino acids identical between the predicted murine and human proteins are indicated by (*).

DNA encoding the murine signal sequence is underlined, with A26 or T27 being the predicted first amino acid of the mature protein.

Please amend the paragraph beginning at page 37, line 3 to read as follows:

A library was constructed λZAP II using ApoI digested genomic DNA from embryonal stem cells and screened with a pool of ^{32}P-labelled oligonucleotides encoding the amino acid sequence Trp-Ser-Asp-Trp-Ser (SEQ ID NO: 12) found in many members of the haemopoietin receptor family. One hybridising bacteriophage clone was found to contain a sequence that appeared to encode part of a novel member of the haemopoietin receptor family. This receptor was given the operational n ame NR4. The sequence of the genomic clone was used to isolate cDNAs encoding NR4 from WEHI-3B cell, peritoneal macrophage, bone marrow, skin and kidney libraries. A composite of the nucleotide sequence (SEQ ID NO: 1) and predicted amino acid sequence (SEQ ID NO: 2) of these cDNAs is shown in Figure 1. The NR4 cDNA is predicte4d to encode for a protein of 424 amino acid residues, containing a putative signal sequence and transmembrane domain. The extracellular region of the protein contained an immunoglobulin-like domain (amino acids 27-117), in addition to a typical haemopoietin receptor domain (amino acids 118-340) which includes four conserved cysteine residues and the characteristic Trp-Ser-Asp-Trp-Ser (SEQ ID NO: 12) motif (Figure 1; in bold as WSXWS). The cytoplasmic tail of the new receptor was 60 amino acids in length.